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(54) Title: ECIST MICROARRAYS FOR DUAL SCREENING OF DNA HYPERMETHYLATION AND GENE SILENCING

(57) Abstract: Novel methods are herein provided for high-throughput, dual analysis of DNA methylation and gene expression, and triple analysis of DNA methylation, gene expression and gene-associated histone acetylation in cancer cells using arrayed expressed CpG island sequence tags (ECISTs). ECISTs correspond to genomic DNA fragments comprising GC-rich segments along with promoter and/or exon (e.g., first exon) portions of genes. The GC-rich segments are useful for screening hypermethylated CpG sites in cancer cells, while the corresponding promoter and exon-containing portions are useful for determining corresponding transcript levels and assessing histone acetylation. Also provided are high-throughput methods for either confirming methylation-dependent gene silencing, or identifying therapeutically effective demethylating agents, using the ECIST array panels to identify hypermethylated loci, and measure expression levels thereof after cellular exposure to demethylating agents. Further provided are high-throughput methods for distinguishing between direct (primary) demethylation-dependent gene up-regulation, and indirect (secondary) demethylation-dependent up-regulation within apparent epigenetic cascades.

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